

An examination of the involvement of proline peptide isomerization in protein folding

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The proline peptide isomerization model of protein folding predicts that the fraction of denatured polypeptide chains which rapidly fold should be quantitatively related to the numbers of cis and trans proline residues in the folded polypeptide conformation. However, we find that neither the comparative nor the absolute kinetic pattern for folding of the homologous proteins, tuna heart and horse heart ferricytochrome c which differ by one proline residue, is compatible with the quantitative predictions of the proline peptide isomerization model. © 1978.